

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 11:53:58 ; Search time 374 Seconds
(without alignments)
101.345 Million cell updates/sec

Title: US-09-824-134-2_COPY_130_245

Perfect score: 593

Sequence: 1 FEAGAAAGAPGEDLCAAF.....QEVOQARDLQNRSGAMSPMS 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	593	100.0	208	14	US-10-207-655-184
2	593	100.0	208	14	US-10-207-655-190
3	593	100.0	211	14	US-10-207-655-408
4	593	100.0	256	9	US-09-933-814-2
5	593	100.0	256	9	US-09-824-134-2
6	593	100.0	256	15	US-10-368-438-2
7	593	100.0	256	17	US-10-923-031-2
8	382.5	64.5	210	14	US-10-207-655-418
9	382	64.4	74	13	US-10-112-793-25
10	382	64.4	74	14	US-10-287-594-5
11	318	53.6	62	13	US-10-035-408-5
12	143.5	24.2	95	11	US-09-972-211-128
13	143.5	24.2	95	15	US-10-087-684-87

14	143.5	24.2	95	15	US-10-218-779-87	Sequence 87, Appl
15	143.5	24.2	95	15	US-10-096-625-128	Sequence 128, Appl
16	143.5	24.2	96	10	US-09-970-944-45	Sequence 45, Appl
17	143.5	24.2	96	15	US-10-037-417-124	Sequence 124, Appl
18	131	22.1	82	15	US-10-087-684-89	Sequence 89, Appl
19	131	22.1	82	15	US-10-218-779-89	Sequence 89, Appl
20	131	22.1	83	10	US-09-970-944-47	Sequence 47, Appl
21	131	22.1	83	15	US-10-037-417-126	Sequence 126, Appl
22	115.5	19.5	656	9	US-09-862-027-30	Sequence 30, Appl
23	111.5	18.8	77	14	US-10-287-594-7	Sequence 7, Appl
24	111.5	18.8	99	15	US-10-359-439-3	Sequence 3, Appl
25	111.5	18.8	100	15	US-10-359-439-1	Sequence 1, Appl
26	111.5	18.8	273	15	US-10-108-260A-3780	Sequence 3780, Ap
27	111.5	18.8	671	9	US-09-758-003-2	Sequence 2, Appl
28	111.5	18.8	671	9	US-09-862-027-29	Sequence 29, Appl
29	111.5	18.8	671	10	US-09-981-397A-16	Sequence 16, Appl
30	111.5	18.8	671	16	US-10-408-765A-2254	Sequence 2254, Ap
31	108.5	18.3	77	13	US-10-112-793-27	Sequence 27, Appl
32	96.5	16.3	396	14	US-10-336-031-1	Sequence 1, Appl
33	86	14.5	294	14	US-10-336-031-2	Sequence 2, Appl
34	86	14.5	400	15	US-10-104-047-2395	Sequence 2395, Ap
35	86	14.5	1762	14	US-10-205-194-117	Sequence 117, Appl
36	86	14.5	3913	15	US-10-334-143-45	Sequence 45, Appl
37	83	14.0	657	14	US-10-186-185-2	Sequence 2, Appl
38	81	13.7	63	13	US-10-035-408-2	Sequence 2, Appl
39	81	13.7	81	14	US-10-287-594-6	Sequence 6, Appl
40	81	13.7	312	14	US-10-207-655-186	Sequence 186, Appl
41	81	13.7	328	15	US-10-296-115-1123	Sequence 1123, Ap
42	79.5	13.4	157	14	US-10-193-934-11	Sequence 11, Appl
43	78.5	13.2	1585	16	US-10-437-963-124349	Sequence 124349
44	78	13.2	104	14	US-10-029-386-30750	Sequence 30750, A
45	78	13.2	199	14	US-10-287-594-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-207-655-184
; Sequence 184, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 184
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-184

Query Match 100.0%; Score 593; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FEAGAAAGAPGEDLCAAFNVICDNVGDWRRLAROLKVSDTKIDSIEDRYPRNLTRV	60
Db	82	FEAGAAAGAPGEDLCAAFNVICDNVGDWRRLAROLKVSDTKIDSIEDRYPRNLTRV	141
Qy	61	RESLRIRWTKENATVAHLVGLRSCNNLVADLVOEQVQARDLQNRSGAMSPMS	116
Db	142	RESLRIRWTKENATVAHLVGLRSCNNLVADLVOEQVQARDLQNRSGAMSPMS	197

RESULT 2

US-10-207-655-190
; Sequence 190, Application US/10207655
; Publication No. US20030118592A1

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; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 190
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-190

Query Match      100.0%; Score 593; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVKGWRRRLARQLKVSQDKIDSIEDRYPRNLTGV 60
    |||||
Db 82 FEAGAAAGAAAGGEEEDLCAAFNVICDNVKGWRRRLARQLKVSQDKIDSIEDRYPRNLTGV 141
    |||||
QY 61 RESLRWKTEKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 116
    |||||
Db 142 RESLRWKTEKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 197
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RESULT 3
US-10-207-655-408
; Sequence 408, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 408
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-408

Query Match      100.0%; Score 593; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 4.1e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVKGWRRRLARQLKVSQDKIDSIEDRYPRNLTGV 60
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Db 85 FEAGAAAGAAAGGEEEDLCAAFNVICDNVKGWRRRLARQLKVSQDKIDSIEDRYPRNLTGV 144
    |||||
QY 61 RESLRWKTEKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 116
    |||||
Db 145 RESLRWKTEKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 200
    |||||

RESULT 4
US-09-933-814-2
; Sequence 2, Application US/09933814
; Patent No. US20020058798A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/09/824,134
; CURRENT FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 814
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-814-2

Query Match      100.0%; Score 593; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAAGGEEEDLCAAFNVICDNVKGWRRRLARQLKVSQDKIDSIEDRYPRNLTGV 60
    |||||
Db 130 FEAGAAAGAAAGGEEEDLCAAFNVICDNVKGWRRRLARQLKVSQDKIDSIEDRYPRNLTGV 189
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QY 61 RESLRWKTEKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 116
    |||||
Db 190 RESLRWKTEKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 245
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RESULT 5
US-09-824-134-2
; Sequence 2, Application US/09824134
; Patent No. US20020082401A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-Apr-2001
; APPLICATION NUMBER: US/09/824,134
; PRIOR APPLICATION DATA:
; FILING DATE: 03-Apr-2001
; APPLICATION NUMBER: 08/860,082
; FILING DATE: <Unknown>
; APPLICATION NUMBER: IL 112022
; FILING DATE: 15-DEC-1994
; APPLICATION NUMBER: IL 112692
; FILING DATE: 19-FEB-1995
; APPLICATION NUMBER: IL 114615
; FILING DATE: 16-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197

```

TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-824-134-2

Query Match 100.0%; Score 593; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 60
DB 130 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 189

QY 61 RESLRWKNTKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 190 RESLRWKNTKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 245

RESULT 6
US-10-368-438-2
Sequence 2, Application US/10368438
Publication No. US20030219411A1
GENERAL INFORMATION:
APPLICANT: David WALLACH
Mark P. BOLDIN
Tanya M. GONCHAROV
Yury V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/368,438
FILING DATE: 20-Feb-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN-1998
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-368-438-2

Query Match 100.0%; Score 593; DB 15; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 60
DB 130 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 189

QY 61 RESLRWKNTKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 190 RESLRWKNTKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 245

RESULT 7
US-10-923-031-2
Sequence 2, Application US/10923031
Publication No. US20050013816A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BOLDIN, Mark
APPLICANT: VAREFOLOMEV, Eugene
APPLICANT: METT, Igor
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL RECEPTORS
FILE REFERENCE: WALLACH-16B
CURRENT APPLICATION NUMBER: US/10/923,031
CURRENT FILING DATE: 2004-08-23
PRIOR APPLICATION NUMBER: US/09/933,814
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 08/860,082
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: PCT/US95/16542
PRIOR FILING DATE: 1995-12-14
PRIOR APPLICATION NUMBER: IL 112022
PRIOR FILING DATE: 1994-12-15
PRIOR APPLICATION NUMBER: IL 112692
PRIOR FILING DATE: 1995-02-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-10-923-031-2

Query Match 100.0%; Score 593; DB 17; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 60
DB 130 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSQTKIDSIEDRYPRNLTERV 189

QY 61 RESLRWKNTKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 116
DB 190 RESLRWKNTKENATVAHLVGLRSCQNLVADLVQEVQQAARDLQNRSGAMSPMS 245

RESULT 8
US-10-207-655-418
Sequence 418, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS


```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/035,408
; FILING DATE: 04-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,626
; FILING DATE: 09-Dec-1997
; APPLICATION NUMBER: IL 112,742
; FILING DATE: 22-FEB-1995
; APPLICATION NUMBER: IL 115,289
; FILING DATE: 13-SEP-1995
; APPLICATION NUMBER: PCT/US96/02326
; FILING DATE: 15-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-035-408-5

Query Match 53.6%; Score 318; DB 13; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.7e-28;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 WRLARQLKVSDFKIDSDIEDYPRNLTERVRESLRWIKNTKENATVAHLVGALRSCQWN 90
DB 1 WRLARQLKVSDFKIDSDIEDYPRNLTERVRESLRWIKNTKENATVAHLVGALRSCQWN 60

QY 91 LV 92
DB 61 LV 62

RESULT 12
US-09-972-211-128
; Sequence 128, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhuseen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding Th
; TITLE OF INVENTION: Methods Of Using The Same

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; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-211-128

Query Match 24.2%; Score 143.5; DB 11; Length 95;
Best Local Similarity 36.2%; Pred. No. 2.2e-08;
Matches 34; Conservative 20; Mismatches 37; Indels 3; Gaps 1;

QY 4 GAAAGAAAGSEEDLCAAPNVICDVGKDWRRRLARQLKVSDFKIDSDIEDYPRNLTERVRES 63
DB 3 GAASLTETREKLA---KLLDHDLDGDDWRELAKLGLSEADIDQIETSPRDLAEQSYQL 59

QY 64 LRIWNTKENATVAHLVGALRSCQWNVLVDLVQ 97
DB 60 LRLWEQREGKNATLTGLTLEALRMGRDDDAVELLR 93

RESULT 13
US-10-087-684-87
; Sequence 87, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.

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Wed Feb 16 07:33:25 2005

; PRIOR APPLICATION NUMBER: 09/972,211
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-096-625-128

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QY	64	LRIWKTEKENATVAHLVGLRSCQNNLVADLVQ	97
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Job time : 374 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 16:41:39 ; Search time 2065 Seconds
(without alignments)
8165.818 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: gb_in.*
- 4: gb_om.*
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- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	348	100.0	627	9	CP456738 Homo sapi
3	348	100.0	627	12	BT007629 Synthetic
4	348	100.0	1642	6	AR317240 Sequence
5	348	100.0	1642	6	AR380940 Sequence
6	348	100.0	1642	6	AR558975 Sequence
7	348	100.0	1642	6	AX774986 Sequence
8	348	100.0	1642	6	AX779974 Sequence
9	348	100.0	1642	9	HSU24231
10	348	100.0	1642	9	HSU74301
11	348	100.0	1701	6	AR211524 Sequence
12	348	100.0	1701	6	AR350946 Sequence
13	348	100.0	1701	9	HSMRNTX
14	348	100.0	1725	9	BC000334
15	346.4	99.5	606	6	BD082771
16	344.8	99.1	606	6	BD082772
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18	307	88.2	456	6	CQ739366 Sequence
19	307	88.2	143409	2	AF001787 Homo sapi

20	307	88.2	169725	9	AP000879
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24	182.6	52.5	1556	10	RNO441127
25	169.2	48.6	1377	10	MMU50406
26	169.2	48.6	1497	10	BC004584
27	169.2	48.6	1512	10	BC021400
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ALIGNMENTS

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LOCUS	BT006927	Complete cds.				
DEFINITION	BT006927.1	GI:30582692				
ACCESSION	BT006927					
VERSION	FLI CDNA.					
KEYWORDS	FLI CDNA.					
SOURCE	FLI CDNA.					
ORGANISM	FLI CDNA.					
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AUTHORS	Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A.					
TITLE	Cloning of human full-length CDSs in BD Creator(TM) System Donor vector					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 627)					
AUTHORS	Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A.					
TITLE	Direct Submission					
JOURNAL	Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA					
COMMENT	This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.					
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[illegible]

QY	301	CAGGCCCGTGACCTCAGACAGGAGTGGGGCCATGTCCCCGATGTCA	348
Db	688	CAGGCCCGTGACCTCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA	735

RESULT 12

AR350946	1701 bp	mRNA	linear	PAT 17-AUG-2003
LOCUS	Sequence 1	from patent US 6586571.		
DEFINITION	AR350946			
ACCESSION	AR350946			
VERSION	AR350946.1	GI:33752607		
KEYWORDS	Source	Unknown.		
ORGANISM	Source	Unknown.		
REFERENCE	1 (bases 1 to 1701)	Unclassified.		
AUTHORS	Wallach,D., Boldin,M., Goncharov,T. and Golstev,Y.V.			
TITLE	Modulators of the function of PAS receptors and other proteins			
JOURNAL	Patent: US 6586571-A 1 01-JUL-2003;			
FEATURES	Location/Qualifiers			
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QY	121	TCAGACACCAAGATTCGACAGCATTCGAGGACAGATACCCCGGCNACTGCACAGAGCGGTGTG	180
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Db	688	CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCTCCCGATGTCA	735
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LOCUS			
DEFINITION			H. sapiens mRNA for mediator of receptor-induced toxicity.
ACCESSION		X84709	
VERSION		X84709.1	GI:791037
KEYWORDS		MORT1 gene.	
SOURCE		Homo sapiens (human)	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE			
AUTHORS		Boldin,M.P., Varfolomeev,E.E., Pancer,Z., Mett,I.L., Camonis,J.H. and Wallach,D.	
TITLE		A novel protein that interacts with the death domain of Fas/APO1 contains a sequence motif related to the death domain	
JOURNAL		J. Biol. Chem. 270 (14), 7795-7798 (1995)	
MEDLINE		95229578	
PUBMED		7536190	
REFERENCE		2 (bases 1 to 1701)	
TITLE		Wallach,D.	
JOURNAL		Direct Submission	
FEATURES		Submitted (10-FEB-1995) D. Wallach, The Weizmann Institute, Dept of Membrane Research & Biophysics, Rehovot 76100, ISRAEL	
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Best Local Similarity		100.0%;	Pred. No. 1.2e-81;
Matches		348; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	TTTCAGAGCGGGCGGGCGGGCGCGCGCTGGGGAAGAACCTGTGTGACGATTTT	60
Db	388	TTTCAGAGCGGGCGGGCGGGCGGGCGCGCTGGGGAAGAACCTGTGTGACGATTT	447
Qy	61	AACGTCATATGTGTAATGTGGGGAAGATTGGAGAGGCTGGCTGCTAGCTCAAAATC	120
Db	448	AACGTCATATGTGTAATGTGGGGAAGATTGGAGAGGCTGGCTGCTAGCTCAAAATC	507
Qy	121	TCAGACCAAGATCGACAGATCGAGACAGATACCCCGACCTGACAGAGCGGTG	180
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Qy	181	CGGGAGTCACAGATCTGGAAGAACACAGAGAGGAGACGCAACAGTGGCCCACTG	240
Db	568	CGGGAGTCACAGATCTGGAAGAACACAGAGAGGAGACGCAACAGTGGCCCACTG	627
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Db	628	GTGGGGGCTCTCAGGTCTCGCAGATGAACCTGGTGGCTGACCTGGTCAAGAGGTTCA	687
Qy	301	CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCTCCCGATGTCA	348
Db	688	CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCTCCCGATGTCA	735
RESULT 14			
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LOCUS			
DEFINITION			Homo sapiens Fas (TNFRSF6)-associated via death domain, mRNA (cDNA clone MGC:8528 IMAGE:2822581), complete cds.
ACCESSION		BC000334	
VERSION		BC000334.2	GI:33875320
KEYWORDS		MGC.	
SOURCE		Homo sapiens (human)	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE			
AUTHORS		1 (bases 1 to 1725)	
TITLE		Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Schuler,G.D., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.B., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalley,D.E., Scherch,A., Schein,J.E., Jones,S.D. and Marra,M.A.	
TITLE		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED		12477932	
REFERENCE		2 (bases 1 to 1725)	
AUTHORS		Strausberg,R.	
TITLE		Direct Submission	
JOURNAL		Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
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		On Aug 19, 2003 this sequence version replaced gi:12653134.	
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		Email: cgapbs-r@mail.nih.gov	
		Tissue Procurement: DCTD/DTP	
		cDNA Library Preparation: Rubin Laboratory	
		DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)	
		Sequencing Center (NISC),	
		Gaithersburg, Maryland:	
		Web site: http://www.nisc.nih.gov/	
		Contact: nisc_mgc@nhgri.nih.gov	
		Akhtar,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maekeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.	
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
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ACCESSION	BD082771	BD082771	Neuronal MORT1 isoforms.				
VERSION	BD082771.1	BD082771.1	GI:22628381				
KEYWORDS	JP 2001522247-A/1.	JP 2001522247-A/1.					
SOURCE	synthetic construct	synthetic construct					
ORGANISM	synthetic construct	synthetic construct					
REFERENCE	1 (bases 1 to 606)	1 (bases 1 to 606)	other sequences; artificial sequences.				
AUTHORS	Bingham,B.W., Young,K.H., Timothy,A., Wood and Birsan,C.	Bingham,B.W., Young,K.H., Timothy,A., Wood and Birsan,C.					
TITLE	Neuronal MORT1 isoforms	Neuronal MORT1 isoforms					
JOURNAL	Patent: JP 2001522247-A	Patent: JP 2001522247-A	1 13-NOV-2001;				

Search completed: February 11, 2005, 19:54:50
Job time : 2071 secs

COMMENT	AMERICAN HOME PRODUCTS CORP
PN	JP 2001522247-A/1
PD	13-NOV-2001
PF	14-APR-1998 JP 1998547026
PR	25-APR-1997 US 60/044835
PI	BRENDAN WILLIAM BINGHAM, KATHLEEN H YOUNG, ANDREW TIMOTHY PI
WOOD, CAMELIA BRIAN	
PC	C12N15/12.C07K14/47.C07K14/715
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Query Match	99.5%; Score 346.4; DB 6; Length 606;
Best Local Similarity	99.7%; Pred. No. 3.1e-81;
Matches 347; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
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Qy 61	AACGTCATATGTGATAATGTGGGGAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
Db 283	AACGTCATATGTGATAATGTGGGGAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 342
Qy 121	TCAGACACCAAGATCGACAGCATCGAGGACATATCCCCCGCAACCTGACAGAGCGTGTG 180
Db 343	TCAGACACCAAGATCGACAGCATCGAGGACATATCCCCCGCAACCTGACAGAGCGTGTG 402
Qy 181	CGGGAGTCACTGAGATCTGGAAGAACACAGAGAAGGAGAACCGCAACAGTGGGCCACCTG 240
Db 403	CGGGAGTCACTGAGATCTGGAAGAACACAGAGAAGGAGAACCGCAACAGTGGGCCACCTG 462
Qy 241	GTGGGGGCTCTCAGTCTCGCAGATGACCTGGTGGCTGACCTGGTACAGAGGTTTCAG 300
Db 463	GTGGGGGCTCTCAGTCTCGCAGATGACCTGGTGGCTGACCTGGTACAGAGGTTTCAG 522
Qy 301	CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
Db 523	CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 570